providing a hybrid polypeptide comprised of an F-box polypeptide and a target polypeptide interaction domain that binds to the target polypeptide; and

contacting the target polypeptide with said hybrid polypeptide,

thereby degrading the target polypeptide.

37. **(New)** The method of claim 36, wherein the hybrid polypeptide binds to the target polypeptide through the target polypeptide interaction domain, thereby recruiting the target polypeptide to an SCF ubiquitin protein ligase complex and causing the ubiquitination of the target polypeptide.

38. **(New)** The method of claim 37, wherein the ubiquitinated target polypeptide further undergoes ubiquitin-dependent proteolysis.

39. **(New)** The method of claim 38, wherein said ubiquitin-dependent proteolysis is by the proteasome.

40. **(New)** The method of claim 36, wherein the F-box polypeptide further comprises a WD domain.

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41. **(New)** The method of claim 36, wherein the F-box polypeptide is selected from the group consisting of Cdc4p, Pop1p, Pop 2p, Grr1p, Met30p, HOSp, beta TrCPp, and FWD1p.

42. **(New)** The method of claim 36, wherein the F-box polypeptide is a polypeptide selected from the group consisting of SEQ ID Nos. 2, 4, 6, 8, 10, and 12.

43. **(New)** The method of claim 36, wherein the F-box polypeptide is encoded by a nucleic acid selected from the group consisting of SEQ ID Nos. 1, 3, 5, 7, 9, and 11.

44. **(New)** The method of claim 36, wherein the F-box polypeptide is at least 70% identical to a contiguous polypeptide sequence of a polypeptide selected from the group consisting of SEQ ID Nos. 2, 4, 6, 8, 10 and 12.

45. **(New)** The method of claim 36, wherein the F-box polypeptide is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID Nos. 1, 3, 5, 7, 9, and 11.

46
~~44~~. **(New)** The method of claim 36, wherein the target polypeptide is targeted for proteolysis in vitro.

47
~~45~~. **(New)** The method of claim 36, wherein the target polypeptide is targeted for proteolysis in vivo.

48
~~46~~. **(New)** The method of claim 36, wherein the target polypeptide interaction domain is selected from the group consisting of a papillomavirus E7 polypeptide, and an SV40 LTP polypeptide.

49
~~47~~. **(New)** The method of claim 36, wherein the target polypeptide is selected from the group consisting of a retinoblastoma polypeptide, a p107 polypeptide, IkB, Sic1p, Cln2p, E2 or beta-catenin.

50
~~48~~. **(New)** A nucleic acid for use in degrading a target polypeptide comprising a hybrid polypeptide-encoding nucleic acid sequence that includes an F-box polypeptide encoding nucleic acid sequence that is functionally linked to a target polypeptide interaction domain-encoding nucleic acid.

51
~~49~~. **(New)** The nucleic acid of claim 48, wherein the F-box polypeptide encoding nucleic acid sequence hybridizes under stringent conditions to a nucleic acid sequence selected from the group consisting of SEQ ID Nos. 1, 3, 5, 7, 9, and 11.

52
~~50~~. **(New)** The nucleic acid of claim 49, wherein the F-box polypeptide encoding nucleic acid sequence is selected from the group consisting of SEQ ID Nos. 1, 3, 5, 7, 9, and 11.